REMARKS

Status of the Claims

Claims 1, 2, 7-19, 24-31 are selected and under prosecution. Claims 3-6 and 20-23 have been withdrawn. Claim 1 and claim 17 have been amended to recite "obtaining information on the functional regions of the genome, using method selection from a group consisting of transcription sites, binding site, origin of replication, and chromatin modification sites; performing a sequence variation detection assay wherein the information is used to design the assay".

Support for the amendment may be found, e.g., on page 27, lines 17-19, page 28, lines 21-23, page 29, lines 1-7 and Figure 1.

The specification is also amended to claim propriety to U.S. application 60/442045.

Applicants assert that no new matter is presented by these amendments and respectfully request entry of the same.

Rejections under 35 U.S.C. § 102 is obviated.

Claims 1, 2, 7, 15, 16, 17, and 24 are rejected under 35 U.S.C. § 102 as allegedly being anticipated by Ren et al. (Science, (2000), volume 290, pages 2306-2309) as allegedly defined by Goffeau et al, (Science, (1996) volume 274, pages 546-567). Applicants respectfully disagree.

However, for the purpose of expediting the issuance of claims, Applicants have amended the claims to recite "obtaining information on the functional regions of the genome, using method selection from a group consisting of transcription sites, binding

site, origin of replication, and chromatin modification sites; performing a sequence variation detection assay wherein the information is used to design the assay." Applicants reserve the rights to pursue the original claims in a related application.

Applicants respectfully submit that the Ren et al. does not disclose a method for interrogating genetic variations by obtaining information on functional regions of the genome, using method selection from a group consisting of transcription sites, binding site, origin of replication, and chromatin modification sites and performing a sequence variation detection assay wherein the information is used to design the assay.

Therefore, Applicants respectfully submit that this rejection of Claims 1, 2, 7, 15, 16, 17, and 24 under 35 U.S.C. § 102 is obviated by the amendment.

Rejections under 35 U.S.C. § 102(e) is obviated.

Claims 1, 2, 7, 15, 16, 17, and 24 are rejected under 35 U.S.C. § 102(e) as allegedly being anticipated by Wyrick et al. (US Patent 6,410,243) as allegedly defined by Goffeau et al, (Science, (1996) volume 274, pages 546-567). Applicants respectfully disagree.

However, for the purpose of expediting the issuance of claims, Applicants have amended the claims to recite "obtaining information on the functional regions of the genome, using method selection from a group consisting of transcription sites, binding site, origin of replication, and chromatin modification sites; performing a sequence variation detection assay wherein the information is used to design the assay." Applicants reserve the rights to pursue the original claims in a related application.

Applicants respectfully submit that the Wyrick et al. does not disclose a method for interrogating genetic variations by obtaining information on functional regions of the genome, using method selection from a group consisting of transcription sites, binding site, origin of replication, and chromatin modification sites and performing a sequence variation detection assay wherein the information is used to design the assay.

Therefore, Applicants respectfully submit that this rejection of Claims 1, 2, 7, 15, 16, 17, and 24 under 35 U.S.C. § 102(e) is obviated by the amendment.

Rejections under 35 U.S.C. § 103(a) should be obviated.

Claims 8-12, 18, 19, and 25-29 are rejected as allegedly being obvious over Ren et al. (Science, (2000), volume 290, pages 2306-2309) as allegedly defined by Goffeau et al, (Science, (1996) volume 274, pages 546-567) allegedly in view of Gentalen et al (US patent 6,306,643). Applicants respectfully disagree.

However, for the purpose of expediting the issuance of claims, Applicants have amended the claims to recite "obtaining information on the functional regions of the genome, using method selection from a group consisting of transcription sites, binding site, origin of replication, and chromatin modification sites; performing a sequence variation detection assay wherein the information is used to design the assay." Applicants reserve the rights to pursue the original claims in a related application.

None of the cited reference, individually or in combination, discloses, suggests or motivates a method for interrogating genetic variations by obtaining information on the functional regions of the genome, using method selection from a group consisting of transcription sites, binding site, origin of replication, and chromatin modification sites;

performing a sequence variation detection assay wherein the information is used to design the assay.

Therefore, Applicants respectfully submit that there is no prima facie obviousness and this rejection of Claims 8-12, 18, 19, and 25-29 under 35 U.S.C. § 103(a) is obviated by the amendment.

Rejections under 35 U.S.C. § 103(a) should be obviated.

Claims 13, 14, 30, and 31 are rejected as allegedly being obvious over Ren et al. (Science, (2000), volume 290, pages 2306-2309) as allegedly defined by Goffeau et al, (Science, (1996) volume 274, pages 546-567) allegedly in view of Gentalen et al (US patent 6,306,643) and allegedly further in view of Rothberg et al (US Patent 5,871,697). Applicants respectfully disagree.

However, for the purpose of expediting the issuance of claims, Applicants have amended the claims to recite "obtaining information on the functional regions of the genome, using method selection from a group consisting of transcription sites, binding site, origin of replication, and chromatin modification sites; performing a sequence variation detection assay wherein the information is used to design the assay." Applicants reserve the rights to pursue the original claims in a related application.

None of the cited reference, individually or in combination, discloses, suggests or motivates a method for interrogating genetic variations by obtaining information on the functional regions of the genome, using method selection from a group consisting of transcription sites, binding site, origin of replication, and chromatin modification sites;

performing a sequence variation detection assay wherein the information is used to design the assay.

Therefore, Applicants respectfully submit that there is no prima facie obviousness and this rejection of Claims 13, 14, 30, and 31 under 35 U.S.C. § 103(a) is obviated by the amendment.

CONCLUSION

For these reasons, Applicants believe all pending claims are now in condition for allowance. If the Examiner has any questions pertaining to this application or feels that a telephone conference would in any way expedite the prosecution of the application, please do not hesitate to call the undersigned at (408) 731-5000.

The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account 01-0431.

Applicants respectfully request that a timely Notice of Allowance be issued in this case.

Respectfully submitted,

October 19, 2006

By _____
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Attachments

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